Appl. No.

10/063,578

Filed

:

May 3, 2002

AMENDMENTS TO THE SPECIFICATION

Please amend the title of the invention as follows:

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS
ENCODING THE SAME ANTIBODIES THAT BIND A PRO1158 POLYPEPTIDE

Please amend the priority statement on page 1, line 2 as follows:

This application is a continuation of, and claims priority under 35 USC §120 to, US Application 10/006867 filed 12/6/2001, which is a continuation of, and claims priority under 35 USC § 120 to, PCT Application PCT/US00/23328 filed 8/24/2000, which is a continuation in part of, and claims priority under 35 USC §120 to, US Application 09/380137 filed 8/25/1999, now abandoned, which is the National Stage filed under 35 USC §371 of PCT Application PCT/US99/12252 filed 6/2/1999, which claims priority under 35 USC §119 to US Provisional Application 60/090246 filed 6/22/1998.

Please amend paragraph [0205], beginning at page 31, as follows:

[0205] Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov the National Institutes of Health website or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

Please amend paragraph [0216] beginning at page 35, as follows:

[0216] Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., <u>Nucleic Acids Res.</u> 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from

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http://www.nebi.nlm.nih.gov the National Institutes of Health website or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.—